--(ii) recovering the multispecific antibody from the host cell culture.--

Please replace the paragraph beginning at page 17, line 16 with the following rewritten paragraph:

--Figs. 2A-2C. Fig. 2A diagrams a selection scheme for $C_{\rm H}3$ heterodimer using phage display vector, pRA2. Phage displaying stable $C_{\rm H}3$ heterodimers are captured using an antibody directed to the gD flag. Fig. 2B diagrams a dicistronic operon in which $C_{\rm H}3$ expressed from a synthetic gene is co-secreted with a second copy of $C_{\rm H}3$ expressed from the natural gene (Ellison et al. Nucleic Acids Res. <u>10</u>:4071-4079 (1982)) as a fusion protein with M13 gene III The synthetic $C_{\tt H}3$ gene is preceded by a sequence encoding a peptide derived from herpes simplex virus glycoprotein D (gD flag, Lasky, L. A. and Dowbenko, D. J. (1984) DNA 3:23-29; Berman, P. W. et al., (1985) Science $\underline{227}$:1490-1492 and a cleavage (G) site for the site-specific protease, Genenase I (Carter, P. et al. (1989) Proteins: Structure, Function and Genetics 6:240-248). Fig. 2C is the nucleic acid sequence of the dicistronic operon (SEQ ID NO:13) of Fig. 2B in which the residues in the translated $C_{\rm H}3$ genes are numbered according to the Eu system of Kabat et al. In Sequences of Proteins of Immunological Interest, 5th ed. vol. 1, pp. 688-696, NIH, Bethesda, MD (1991). Protuberance mutation T366W is shown, as are the residues targeted for randomization in the natural $C_{H}3$ gene (366, 368, and 407).--

Please replace the paragraph beginning at page 96, line 8 with the following rewritten paragraph:

--A large human single chain Fv (scFv) antibody library (Vaughan et al. (1996), supra) was panned for antibodies specific for eleven antigens including Axl(human receptor tyrosine kinase ECD), GCSF-R (human granulocyte colony stimulating factor receptor

ECD), IgE (murine IgE), IgE-R (human IgE receptor α -chain), MPL (human thrombopoietin receptor tyrosine kinase ECD), MusK (human muscle specific receptor tyrosine kinase ECD), NpoR (human orphan receptor NpoR ECD), Rse (human receptor tyrosine kinase, Rse, ECD), HER3 (human receptor tyrosine kinase HER3/c-erbB3 ECD), Ob-R (human leptin receptor ECD), and VEGF (human vascular endothelial growth factor) where ECD refers to the extracellular domain. The nucleotide sequence data for scFv fragments from populations of antibodies raised to each antigen was translated to derive corresponding protein sequences. The $V_{\scriptscriptstyle L}$ sequences were then compared using the program "align" with the algorithm of Feng and Doolittle (1985, 1987, 1990) to calculate the percentage identity between all pairwise combinations of chains (Feng, D.F. and Doolittle, R.F. (1985) J. Mol. Evol. <u>21</u>:112-123; Feng, D.F. and Doolittle, R.F. (1987) J. Mol. Evol. <u>25</u>:351-360; and Feng, D.F. and Doolittle, R.F. (1990) Methods Enzymol. <u>183</u>:375-387). The percent sequence identity results of each pairwise light chain amino acid sequence comparison were arranged in matrix format (Table 6.1-6.15).

On page 107, after line 29 and before line 30, insert Table 6.1-6.15:

TABLE 6.3

TABLE 6.5

TABLE 6.6

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TABLE 6.9

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